



Alignment of human (query 1) and hamster (Sbjvt 1) SKI-1/S1P

Query: 1 MKLVNIWLLLLLVLLCGKKHLGDRLEKKSFEKAPCPGCSHLTLKVEFSSTVVEYIYIVAF 60
MKL+NIWLLLLLVLLCGKKHLGDRL KK+FEKA CP CSHLTLKVEFSSTVVEYIYIVAF
Sbjct: 1 MKLINIWLLLLLVLLCGKKHLGDRLGKKA FEKASCPSCSHLTLKVEFSSTVVEYIYIVAF 60

Query: 61 NGYFTAKARNSFISSALKSSEVDNWRIIPRNNPSSDYPSPDFEVIQIKEKQKAGLLTLEDH 120
NGYFTAKARNSFISSALKSSEVDNWRIIPRNNPSSDYPSPDFEVIQIKEKQKAGLLTLEDH
Sbjct: 61 NGYFTAKARNSFISSALKSSEVDNWRIIPRNNPSSDYPSPDFEVIQIKEKQKAGLLTLEDH 120

Query: 121 PNIKRVTPORKVFRSLKYAESDPTVPCNETRWSQKWQSSRPLRRASLSLGS GFWHATGRH 180
PNIKRVTPORKVFRSLK+AESDP VPCNETRWSQKWQSSRPLRRASLSLGS GFWHATGRH
Sbjct: 121 PNIKRVTPORKVFRSLKFAESDPIVPCNETRWSQKWQSSRPLRRASLSLGS GFWHATGRH 180

Query: 181 SSRLLRAIPRQVAQTLQADVLWQMGYTGANVRVAVFDTGLSEKHPHFKNVKERTNWTNE 240
SSRLLRAIPRQVAQTLQADVLWQMGYTGANVRVAVFDTGLSEKHPHFKNVKERTNWTNE
Sbjct: 181 SSRLLRAIPRQVAQTLQADVLWQMGYTGANVRVAVFDTGLSEKHPHFKNVKERTNWTNE 240

Query: 241 RTLDDGLGHGTFVAGVIAS MRECQGFAPDAELHIFRVFTNNQVSYTSWFLDAFN YAILKK 300
RTLDDGLGHGTFVAGVIAS MRECQGFAPDAELHIFRVFTNNQVSYTSWFLDAFN YAILKK
Sbjct: 241 RTLDDGLGHGTFVAGVIAS MRECQGFAPDAELHIFRVFTNNQVSYTSWFLDAFN YAILKK 300

Query: 301 IDVLNLSIGGPDFMDHPFVDKVWELTANNVIMVSAIGNDGPLYGTLNNPADQMDVIGVGG 360
IDVLNLSIGGPDFMDHPFVDKVWELTANNVIMVSAIGNDGPLYGTLNNPADQMDVIGVGG
Sbjct: 301 IDVLNLSIGGPDFMDHPFVDKVWELTANNVIMVSAIGNDGPLYGTLNNPADQMDVIGVGG 360

Query: 361 ID FEDNIARFSSRGM TTWELPGGYGRMKPDI VTYGAGVRGSGVKGGCRALSGTSVASPVV 420
ID FEDNIARFSSRGM TTWELPGGYGR+KPDIVTYGAGVRGSGVKGGCRALSGTSVASPVV
Sbjct: 361 ID FEDNIARFSSRGM TTWELPGGYGRVKPDI VTYGAGVRGSGVKGGCRALSGTSVASPVV 420

Query: 421 AGAVTLLVSTVQKREL VNPASMKQALIASARRLP GVMNMF EQGHGKLDLLRAYQILNSYKP 480
AGAVTLLVSTVQKREL VNPAS+KQALIASARRLP GVMNMF EQGHGKLDLLRAYQIL+SYKP
Sbjct: 421 AGAVTLLVSTVQKREL VNPASVKQALIASARRLP GVMNMF EQGHGKLDLLRAYQILSSYKP 480

Query: 481 QASLSPSYIDLTECPYMWPYCSQPIYYGGMPTVVNVTILNMGV TGRIVDKPDWQPYLPQ 540
QASLSPSYIDLTECPYMWPYCSQPIYYGGMPT+VNV TILNMGV TGRIVDKP+W+PYLPQ
Sbjct: 481 QASLSPSYIDLTECPYMWPYCSQPIYYGGMPTIVNV TILNMGV TGRIVDKPEWRPYLPQ 540

Query: 541 NGDNIEVAFSYSSVLWPWSGYLAISISVT KKAASWEGIAQGHVMITVASPAETESKNGAE 600
NGDNIEVAFSYSSVLWPWSGYLAISISVT KKAASWEGIAQGH+MITVASPAETE+KNGAE
Sbjct: 541 NGDNIEVAFSYSSVLWPWSGYLAISISVT KKAASWEGIAQGHIMITVASPAETEAKNGAE 600

Query: 601 QTSTVKLPIKVKI IPTPPRSKRVLWDQYHNLRYP PGYFPRDNLRMKN DPLDWN GDHHTN 660
TSTVKLPIKVKI IPTPPRSKRVLWDQYHNLRYP PGYFPRDNLRMKN DPLDWN GDH+HTN
Sbjct: 601 HTSTVKLPIKVKI IPTPPRSKRVLWDQYHNLRYP PGYFPRDNLRMKN DPLDWN GDHVHTN 660

Query: 661 FRDMYQHLRSMGYFVEVLGAPFTCFDASQYGTLLMVDSEEEYFP EEIAKLRRD VDNGLSL 720
FRDMYQHLRSMGYFVEVLGAPFTCFDA+QYGTLLMVDSEEEYFP EEIAKLRRD VDNGLSL
Sbjct: 661 FRDMYQHLRSMGYFVEVLGAPFTCFDATQYGTLLMVDSEEEYFP EEIAKLRRD VDNGLSL 720

Query: 721 VIFSDWYNTSVMRKVKFYDENTRQWWMPDTGGANIPALNELLSVWNMGFS DGLYEGEFTL 780
VIFSDWYNTSVMRKVKFYDENTRQWWMPDTGGANIPALNELLSVWNMGFS DGLYEGEF L
Sbjct: 721 VIFSDWYNTSVMRKVKFYDENTRQWWMPDTGGANIPALNELLSVWNMGFS DGLYEGEFAL 780

Query: 781 ANHDMYYASGCSIAKFPEDGVVITQT FDKDQGLEVLKQETAVVENVPILGLYQIPAE GGGGR 840

Sbjct: 781 ANHDMYYASGCSIAKFPEDGVVITQTFKDQGLEVLKQETAVVENVPILGLYQIPAEGGGR 840

Query: 841 IVLYGDSNCLDDSHRQKDCFWLLDALLQYTSYGVTPPSLSHSGNRQRPPSGAGSVTPERM 900
IVLYGDSNCLDDSHRQKDCFWLLDALLQYTSYGV PPSLSHSGNRQRPPSGAG PERM

Sbjct: 841 IVLYGDSNCLDDSHRQKDCFWLLDALLQYTSYGVNPPSLSHSGNRQRPPSGAGLAPPERM 900

Query: 901 EGNHLHRYSKVLEAHLGDPKPRPLPACPRLSWAKPQPLNETAPSNLWKHQKLLSIDLDKV 960
EGNHLHRYSKVLEAHLGDPKPRPLPACP LSWAKPQPLNETAPSNLWKHQKLLSIDLDKV

Sbjct: 901 EGNHLHRYSKVLEAHLGDPKPRPLPACPHLSWAKPQPLNETAPSNLWKHQKLLSIDLDKV 960

Query: 961 VLPNFRSNRPQVRPLSPGESGAWDIPGGIMPGRYNQEVGQTIPVFAFLGAMVVLAFFVVQ 1020
VLPNFRSNRPQVRPLSPGESGAWDIPGGIMPGRYNQEVGQTIPVFAFLGAMV LAFFVVQ

Sbjct: 961 VLPNFRSNRPQVRPLSPGESGAWDIPGGIMPGRYNQEVGQTIPVFAFLGAMVALAFFVVQ 1020

Query: 1021 INKAKSRPKRRRPRAKRPQLMQQVHPPKTPSV 1052
I+KAKSRPKRRRPRAKRPQL QQ HPP+TPSV

Sbjct: 1021 ISKAKSRPKRRRPRAKRPQLTQQTHPPRTPSV 1052